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Delete the paragraph at page 3, lines 14-25 and insert the following paragraph:

In one embodiment, this invention provides an isolated nucleic acid comprising a nucleic acid selected from the group consisting of a nucleic acid encoding any one of Blm open reading frames (ORFs) 8 through 41, and/or a nucleic acid encoding a polypeptide encoded by any one of Blm open reading frames (ORFs) 8 through 41, and/or a nucleic acid amplified by polymerase chain reaction (PCR) using any one of the primer pairs identified in Table II and the nucleic acid of a bleomycin-producing organism as a template. The nucleic acid may comprise one or multiple (e.g. two, more preferably 3 or more) bleomycin open reading frames (i.e. BLM ORFs 8 through 41). One preferred nucleic acid comprises a nucleic acid encoding a C domain lacking one or more His residues of the conserved HHxxxDG (SEQ ID NO:4) active site for transpeptidation. In another preferred embodiment the nucleic acid comprises a nucleic acid encoding a protein encoded by a gene selected from the group consisting of blmI, blmII, and blmXI.

Delete the paragraphs at page 15, lines 18-31 and insert the following:

Figure 8A shows a restriction map of the *blm* gene cluster from *Sv* ATCC15003 (B, *Bam*HI). 8B shows the relative position of the *blmI*, *blmII*, and *blmXI* genes to the two *blmAB* resistance genes (*blm^R*, Blm resistance). Individual open reading frames are represented by open arrows. Figure 8C (SEQ ID NO:127 & 128) shows the nucleotide sequence of the *blmI* gene. The potential ribosome-binding site (RBS) and the conserved motif for **-phosphopantetheinylation are underlined. The sequence has been deposited into GenBank under accession no. AF210249.

Figure 9 shows an amino acid sequence comparison of BlmI (SEQ ID NO:133) with PCP domains of known type I NRPSs (Grs-2 [P14688] (SEQ ID NO:129), 36% identity, 58% similarity; Srfa-3 [Q08787] (SEQ ID NO:130), 40% identity, 64% similarity; Vir-s [Y11547] (SEQ ID NO:131), 36% identity, 60% similarity; Saf-b [U24657] (SEQ ID NO:132), 40% identity, 54% similarity). Given in brackets are nucleotide sequence accession numbers. The shaded letters indicate similar amino acids. Consensus residues are amino acids that are similar in more than three sequences. The signature motif for 4'-phosphopantetheinylation is underlined.-

Delete the paragraph at page 68, line 8 through page 69, line 16 and insert the following:

The similarities among PPTases from different organisms are reduced to two short motifs separated by 40-45 residues: (V/I)G(V/I)D (SEQ ID NO:87), and (F/W)(S/C/T)XKE(A/S)hhK (SEQ ID NO:91) (Lambalot et al. Chem. Biol. (1996) 3:923-936; Walsh etal. Curr. Opin. Chem. Biol. (1997)

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1:309-315). Our previous attempts to amplify PPTase sequences from S. verticillus chromosomal DNA using degenerate primers according to the two conserved motifs were unsuccessful (unpublished results), so we decided to narrow our target. PPTases have been classified in two groups, according to their specificity for the carrier-protein substrate: PPTases involved in polyketide/fatty acid biosynthesis use acyl carrier proteins (ACPs) as substrate, while those for non-ribosomal peptide biosynthesis use peptidyl carrier proteins (PCPs) or aryl carrier proteins (ArCPs) (Walsh et al. Curr. Opin. Chem. Biol. (1997) 1:309-315). Several "NRPS-type" PPTase sequences were used to screen the databases to look for actinomycete homologues, and four proteins of unknown function were found: NshC from Streptomyces actuosus (Li et al. Gene (1990) 91:9-17), SC5A7. 23 from S. coelicolor (GenBank AL031107), an unnamed protein from Streptomyces sp. strain TH1 (Mori et al. J. Bacteriol. (1997) 179:5677-5683), and Rv2794c (later renamed PptT (Quadri et al. Chem. Biol. (1998) 5:631-645)) from Mycobacterium tuberculosis (GenBank AL008967). The alignment of the actinomycete sequences showed the two motifs conserved in all PPTases and an additional motif - the "THC" motif: PXWPXGX2GS(M/L)THCXGY (SEQ ID NO:86), located about 15 amino acids upstream of the (V/I)G(V/I)D motif (SEQ ID NO:87). The "THC" motif is not universally conserved in all PPTases, but it can be detected also in some nonactinomycete PPTases like EntD (Coderre et al. J. Gen. Microbiol. (1989) 135:3043-3055). Using a recently developed method of PCR primer design (the CODEHOP strategy (COnsensus-DEgenerate Hybrid Oligonucleotide Primer) (Rose et al. Nucleic Acids Res. (1998) 26:1628-1635), two primers were designed around the typical C-terminal PPTase motif (primers KEA-1: 5'-T GCA GCA GAA CAG GAG GCK NYC CCA NKG-3' (SEQ ID NO:88) and KEA-2: 5'-TG GGT CAG CGG GTA CCA NRC YTT RWA-3' (SEQ ID NO: 89, H=C+A, N=A+C+T+G, Y=C+T, K=G+T, R=A+G, W=T+A)), and one primer was designed from the "THC" motif (primer THC: 5'-C GGC ATG GTC GGC TCC HTN ACN CAY TG-3', SEQ ID NO:90, H=C+A, N=A+C+T+G, Y=C+T, K=G+T, R=A+G, W=T+A); this motif is not universally conserved in PPTases of all organisms). Using S. verticillus chromosomal DNA as template, no amplification product was detected using the THC and the KEA-1 primers. The set of primers THC/KEA-2 successfully amplified a single band of the expected size (about 250 bp), which was gelpurified and cloned. Eight individual clones were sequenced, and all of them resulted to be identical (except differences due to primer utilization) and highly similar to the putative actinomycete PPTases. The PCR fragment was used as a probe to screen a S. verticillus genomic library by colony hybridization. Of the 10,000 colonies screened, 25 positive clones were identified, and then confirmed by Southern analysis

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to contain the same 4. 6-kb BamHI hybridizing band. The 4. 6-kb DNA fragment was subcloned, and the nucleotide sequence of a 1,761-bp BamHI-SalI region was determined (SEQ ID NO. 3).--

Delete the paragraph on page 69, line 17 through page 70, line 20 and insert the following:

-- The sequence of the 1,761-bp BamHI-SalI fragment was analyzed for coding regions by using the CODONPREFERENCE and TESTCODE programs of the GCG package (Genetics Computer Group, Madison, Wisconsin). Two complete ORFs (pptA, orf3) and two incomplete ORFs (orf1, orf4) were identified within the sequenced region (Figure 13). The first ORF from left to right (designated orf1) starts out of the analyzed area and ends with a TGA codon at position 248 of the sequenced fragment. Comparison of the deduced product of orf1 with proteins in databases showed similarities with Rv2795c from Mycobacterium tuberculos's (GenBank AL008967) and SC5A7. 22 from S. coelicolor (GenBank AL031107), both of unknown function. The second ORF, pptA, contains the sequence amplified by PCR and used for the cloning of this locus. It comprises 741 nucleotides, starting with a GTG codon (position 245) which is coupled to the stop codon of orf1, and ending with a TAA codon. The starting codon of pptA is preceded by a potential ribosomal binding site (RBS), GGGAG. The overall (76.6%) and third codon position (93. 9%) G+C contents and the codon usage of pptA are similar to those found in other Streptomyces genes, with the exception of the stop codon (TAA), which is most uncommon in this group of organisms (Wright et al. Gene (1992) 113:55(65). The pptA gene encodes a protein of 246 amino acids with a predicted molecular mass of 25,619 Da and a pI of 4. 76, which contains the conserved PPTase motifs. Databases searches with PptA showed significant similarities to the putative actinomycete PPTases (39-52%/48-61% identity/similarity) and to confirmed bacterial PPTases such as EntD from E. coli (17%/24% identity/similarity) (Lambalot et al. Chema. Biol. (1996) 3:923-936). The third ORF, orf3, is separated from pptA by an apparently noncoding DNA region of 153 bp, and it is transcribed in opposite and convergent direction with respect to orf1-pptA. The gene orf3 comprises 240 nucleotides, starting with an ATG codon (position 1358) and ending with TGA. The starting codon of orf3 is preceded by the sequence GAAGG, a potential RBS. The deduced product of orf3 encodes a protein of 79 amino acids with a predicted mass of 7,555 Da and a pI of 7. 17. The Orf3 protein shows similarities to the N-terminal region of SC5H1. 35c, a protein of unknown function from S. coelicolor (GenBank AL049863). Analysis of Orf3 with the SignalP program (Nielsen et al. Protein Engineer) (1997) 10:1-6) predicts an N-terminal signal peptide which would be cleaved between residues 27 and 28 (ALA-DS), suggesting that the mature protein (52 amino acids, 5,099 Da, pI 4. 31) would be secreted. Between orf3 and orf4 there is an

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apparently noncoding region of 251 nucleotides. The *orf4* gene is transcribed in opposite and divergent direction with respect to *orf3*. It starts with an ATG codon at position 1610, preceded by a potential RBS (GGAGG), and ends out of the sequenced fragment. The deduced protein product (50 amino acids) of the incomplete *orf4* contains a potential NAD/FAD binding motif, GXGX₂GX₃GX₆G (SEQ ID NO:92) (Scrutton et al. *Nature* (1990) 343:38-43), showing low similarities to diverse oxidoreductases.--

At pages 21-23, delete Table II and insert the following replacement Table II:

Table II. Blm gene cluster open reading frames (ORFs) and primers for ORF amplification.

Orf-8	Orf#	Position	Activity	Method	Primers	Seq
orf-8 SEQ ID NO:115 SEQ ID NO:115 SEQ ID NO:115 SEQ ID NO:115 Oxigase orf-9 ADP-heptose synthase orf-10 SEQ ID NO:114 ADP-heptose synthase Oxidase Orf-10 SEQ ID NO:113 ADP-heptose synthase Oxidase Orf-10 SEQ ID NO:113 ADP-heptose synthase Oxidase					Forward	ID
SEQ ID NO:115 77457 coproporphyrinogen III oxidase orf-9 74690- ADP-heptose synthase (blmC) comparison¹ R: TCATGGGGGGCCCC 7 SEQ ID NO:114 76186 (blmC) comparison¹ R: TCATGGGGTGCCCC 7 SEQ ID NO:113 74693 (blmL) Expression and biochemical characterization.² R: TCATGGGGTGCCGCGGGGC 9 SEQ ID NO:113 74693 (blmL) Expression and biochemical characterization.² R: TCATGGGGTCCGGCGGGC 9 SEQ ID NO:112 74424 (blmD) Gapped-blast comparison¹ R: TCATGAGCGCCCGGCGCCCC 10 orf-12 71618- ADP-heptose LPS heptosyl Gapped-blast comparison¹ R: TCATGAGCGGCCCGTCC 11 SEQ ID NO:111 72790 transferase (blmE) comparison¹ R: TCATGAGCGGCCCGTTCC 13 SEQ ID NO:110 71546 synthesis of mycobactin comparison¹ R: TCATGAGCACCCCATGAC 13 SEQ ID NO:109 70986 (condensation, blml/I) comparison¹ R: TCAGGTGCCCGGACACGCG 15 SEQ ID NO:109 70986 (condensation, blml/I) comparison¹ R: TCATGACCCCCCGGCACA 17 SEQ ID NO:108 69601 of syrP) Comparison¹ R: TCATCGGTGCCCCCGGCACA 17 SEQ ID NO:107 68585 oxidase (NRPS-0, blml/II) comparison¹ R: TCACGGGGCCCCCCGGCCC 19 SEQ ID NO:106 65781 (NRPS-2-1,blmIV) Expression and bochemical characterization.² orf-18 55899- Asparagine synthetase SEQ ID NO:105 57815 orf-19 54418- Homolog of hydroxylase-dehydrogenase (blmF) comparison¹ R: TCACGCACCCCTCGCCC 26 Orf-20 53427- Nucleotide-sugar epimerase Gapped-blast F: GTGACCACCCCCTCCC 29 Orf-20 53427- Sepoile No:103 54404 (blmC) comparison¹ R: TCACGCGGCACCCCC 31 Sapped-blast F: GTGACCACCCCCTCCC 26 Capped-blast F: GTGAGCCCCCCGTGCCC 26 Capped-blast F: GTGAGCCCCCCGCCC 27 Capped-blast F: GTGAGCACCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC					Reverse	No.
orf-9 74690- ADP-heptose synthase Gapped-blast F: GTGAACACCGACCTGCCC 7 SEQ ID NO:114 76186 (bmC) comparison¹ R: TCATGGGGTGTCTCCCT 8 Orf-10 74421- SEQ ID NO:113 74693 (blm) comparison¹ Characterization.² orf-11 72787- Carbamy transferase Gapped-blast characterization.² orf-12 71618- ADP-heptose LPS heptosyl transferase (blmE) comparison¹ R: TCATGAGCGGCCCGGTGCC 12 Orf-13 70983- Homolog of mbft in the SEQ ID NO:110 71546 synthesis of mycobactin comparison¹ R: TCATGAGCGCCCCGGGGG 16 orf-14 69598- Peptide synthetase (condensation, blmll) comparison¹ R: TCATGAGCGCCCCCGGG 16 orf-15 68582- Regulatory gene (homolog Gapped-blast Comparison¹ R: TCATCGGTGCCCGCACA 17 SEQ ID NO:108 69601 of syrP) comparison¹ R: TCACGGGCCCCCCGGCACA 17 SEQ ID NO:107 68585 oxidase (NRPS-0, blmlll) comparison¹ R: TCACGCGCTCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC	orf-8	76183-	Oxygen-independent	Gapped-blast	F: ATGAGCCACGCCATCGGA	5
orf-9 SEQ ID NO:11474690- 76186 (OkmC)ADP-heptose synthase (OkmC)Gapped-blast comparisonF: GTGAACACCGACCTGCCC R: TCATGGGGTTCTCCCTC7orf-10 SEQ ID NO:11374421- 74693Pepudyl carrier protein (blml)Expression and biochemical characterization.2F: ATGACCGCCCCGGGGGC R: TCACCGGTCCCCCCCCCCC10orf-11 SEQ ID NO:112 Orf-12 Orf-12 Tof-13 TOF-13 TOF-14 TOF-14 TOF-14 TOF-14 SEQ ID NO:110ADP-heptose LPS heptosyl transferase (blbE) Transferase (blbE) (condensation, blmII)Gapped-blast Comparison Comparison Comparison R: TCATGAGCGGCCCCCCCGCGG R: TCATGAGCGGCCCCCCCGCGG R: TCATGAGCGGCCCCCCCGCGG R: TCATGAGCGGCCCCCCCGCGG R: TCATGAGCGGCCCCCCCGCGG R: TCATGAGCGGCCCCCCCGCGG R: TCATGAGCGGCCCCCCCCGCGG R: TCATGAGCGGCCCCCCCGCGG R: TCATGAGCGGCCCCCCCGCGG R: TCATGAGCGGCCCCCCCGCGG R: TCATGAGCGGCCCCCCGCGG R: TCATGAGCGGCCCCCCGCGG R: TCATGAGCGCCCCCCGCGG R: TCATGAGCGCCCCCCGCGCC R: TCATGAGCGCCCCCCGCGC R: TCACCGGCTCCGCCC R: TCATCGGTGCCCCCCGCGCC R: TCATCGGTGCCCCCCGCGCC R: TCATCGGTGCCCCCCCCCCGCGCC R: TCACCGGCTCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC	SEQ ID NO:115	77457	coproporphyrinogen III	comparison	R: TCAGGCGCGTTCGGGGGC	6
SEQ ID NO:114 76186 (bmC) comparison R: TCATGGGGTGTCTCCTC 8 orf-10 74421 Pephidyl carrier protein Expression and biochemical characterization. F: ATGAGCGCCCGGGGGGC 9 protein Comparison R: TCACGGGTCCCCCCCCC 10 protein Comparison R: TCACGGGTCCCCCCCC 10 protein Comparison R: TCATGAGCGCCCGCGGGGCC 10 protein Comparison R: TCATGAGCGCCCCGTCCC 11 protein Comparison R: TCATGAGCGGCCCCGTCC 12 protein Comparison R: TCATGAGCGGCCCCGTCC 12 protein Comparison R: TCATGAGCGGCCCCCGTCC 12 protein Comparison R: TCATGAGCGGCCCCCGTGCC 12 protein Comparison R: TCATGAGCGGCCCCCGGG 13 protein Comparison R: TCATGAGCGTACCCCCATGACC 14 protein Comparison R: TCATGAGCGTACCCCCATGACC 14 protein Comparison R: TCATGAGCGTACCCCCGGGG 15 protein Comparison R: TCATGGGGTACTCTGAT 14 protein Comparison R: TCATGGGGTACTCCTGAT 14 protein Comparison R: TCATGGTGCCGGCACCGGGGGCCCCCGGGACA 17 protein Comparison R: TCATGGTGCCCCCCGGGACA 17 protein Comparison R: TCATGGTGCCCCCCGGGACA 17 protein Comparison R: TCATGGTGCCCCCCGGGACCCCCCGGACA 17 protein Comparison R: TCATGGTGCCCCCCGGCACCCCCCCGGACA 17 protein Comparison R: TCACGCGCCCCCGGCCC 19 protein Comparison R: TCACGCGCCCCCCGGCCC 19 protein Comparison R: TCACGGGGCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC	•	`	oxidase	_		
SEQ ID NO:113 74421- Pepidyl carrier protein Sex pression and biochemical characterization. R: TCACGGGTCCCGCTCCCC 10 Tof-11 T2787- Carbamykransferase Gapped-blast comparison R: TCATGACGGCCCCGTCCCC 11 T2787- T2787- Carbamykransferase Gapped-blast comparison R: TCATGACGGCCGCCCCT 12 T12 T1618- ADP-heptose LPS heptosyl transferase (blnE) Comparison R: TCATGACCCCCATGACC 13 T2790 Transferase (blnE) Comparison R: TCATGACCCCCCATGACC 13 T2790 Transferase (blnE) Comparison R: TCATGACCCCCCATGACC 14 T2790 Transferase (blnE) Comparison R: TCATGACCCCCCATGACC 15 TCATGACCCCCCATGACC T2 T2 T2790 Transferase (blnE) Comparison R: TCATGACCACCCCCATGACC T3 TCATGACTACCCCCCATGACC T3 TCATGACTACCCCCCATGACC T4 TCATGACTACCCCCCATGACC T5 TCATCACTACCCCCCATGACC T5 TCATCACTACCACCCCCCATGACC T5 TCATCACTACCACCCCCCCCCCCCCCCCCCCCCCCCC	orf-9	74690-	ADP-heptose synthase	Gapped-blast	F: GTGAACACCGACCTGCCC	7
SEQ ID NO:113 74421- Pepidyl carrier protein Expression and biochemical characterization. F: ATGAGGGCCCGGGGGC 9	SEQ ID NO:114	76186	(blmC)	comparison	R: TCATGGGGTGTCTCCCTC	8
SEQ ID NO:113 74693 (b/ml) biochemical characterization. ² R: TCACCGGTCCCGCTCCCC 10	orf-10	74421-		Expression and	F: ATGAGCGCCCCGCGGGC	9
orf-11 72787- Carbamytransferase Gapped-blast F: ATGACGCCGACCCGTCC 11 SEQ ID NO:112 74424 (blmD) comparison¹ R: TCATGAGGGCGCGCCGT 12 orf-12 71618- ADP-heptoscLPS heptosyl transferase (blmE) comparison¹ R: TCATGAGGGGCCCCATGACC 13 SEQ ID NO:111 72790 transferase (blmE) comparison¹ R: TCATGAGGGTACTCCTGAT 14 orf-13 70983- Homolog of mbtH in the Sapped-blast comparison¹ R: TCATGGGGTACTCCTGAT 14 orf-14 69598- Peptide synthetase (condensation, blmII) comparison¹ R: TCATGGGGTACCCCCGGGG 16 orf-14 69598- Peptide synthetase (condensation, blmII) comparison¹ R: TCATCGGTGGCCCCCGGGACAC 17 SEQ ID NO:109 70986 (condensation, blmII) comparison¹ R: TCATCGGTGGCCCCCGGGACAC 17 SEQ ID NO:108 69601 of syrP) comparison¹ R: TCACGGGGCCCCCCGGCCC 19 orf-16 65778- Mutated peptide synthetase- Oxidase (NRPS-0, blmIII) comparison¹ R: TCACGGGGCCCCCGGCCC 21 SEQ ID NO:106 65781 (NRPS-2-1,blmIV) biochemical characterization.² orf-18 55899- SEQ ID NO:105 57815 comparison¹ R: TCACGCGCCCCGGCCC 24 orf-19 54418- Homolog of hydroxylase- Gapped-blast comparison¹ R: TCACGCGCCCCGGCCC 26 orf-20 53427- Nucleotide-sugar epimerase Gapped-blast comparison R: TCACGCGCCCCGGCC 28 orf-21 51493- Peptide synthetase Gapped-blast F: GTGACGACCCCTCCC 30 orf-21 51493- Peptide synthetase Gapped-blast Comparison R: TCACGCGCCCCGGCCC 30 orf-21 51493- Peptide synthetase Gapped-blast Comparison R: TCACTCCCCGGTCCCC 30 orf-21 51493- Peptide synthetase Gapped-blast Comparison R: TCACGCACCGTTGCCCC 30 orf-21 51493- Peptide synthetase Gapped-blast Comparison R: TCACGCACCGTCCCCCC 30	SEQ ID NO:113	74693	(blm)	biochemical	R: TCACCGGTCCCGCTCCCC	10
orf-11 72787- Carbamytransferase Gapped-blast comparison¹ R: TCATGAGGGGCCGCGTC 12	`		` \	characterization. ²		
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orf-12 71618- ADP-heptose LPS heptosyl SEQ ID NO:111 72790 transferase (blnE) comparison¹ R: TCATGGGGTACTCCTGAT 14 orf-13 70983- Homolog of mbH in the Sex of mycobactin comparison¹ R: TCAGGGGCCCCGGGG 15 SEQ ID NO:110 71546 synthesis of mycobactin comparison¹ R: TCAGGTGCCGACACGGG 16 orf-14 69598- Peptide synthetase (condensation, blmII) comparison¹ R: TCATGGTGCCGGACACGGG 16 orf-15 68582- Regulatory gene (homolog of syrP) comparison¹ R: TCATCGGTGCCCCCGGCACA 17 SEQ ID NO:108 69601 of syrP) comparison¹ R: TCACGGGCCCCCGGCACA 18 SEQ ID NO:108 69601 of syrP) comparison¹ R: TCACGGGCCCCCGGCCC 19 orf-16 65778- Mutated peptide synthetase oxidase (NRPS-0, blmIII) comparison¹ R: TCACGGGGCCCCGGCCC 21 SEQ ID NO:106 65781 (NRPS-2-1,blmIV) bochemical characterization.² orf-18 55899- Asparagine synthetase Gapped-blast comparison¹ R: TCACCGGCCCCCGCCC 24 SEQ ID NO:105 57815 comparison¹ R: TCACCGGGTCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC	SEQ ID NO:112	74424	(blmD)	comparison	R: TCATGAGCGGGCCGCCGT	12
SEQ ID NO:111 72790 transferase (bln E) comparison R: TCATGGGGTACTCCTGAT 14 orf-13 70983- Homolog of mblt in the synthesis of mycobactin comparison R: TCAGGTGCCGGACACGCG 15 SEQ ID NO:110 71546 synthesis of mycobactin comparison R: TCAGGTGCCGGACACGCG 16 orf-14 69598- Peptide synthetase (condensation, blmll) comparison R: TCATCGGTGCCCCCGGCACA 17 SEQ ID NO:109 70986 (condensation, blmll) comparison R: TCATCGGTGGCTCCTGT 18 orf-15 68582- Regulatory gene (homolog of syrP) comparison R: TCACGCGCTCACCTCGT 20 orf-16 65778- Mutated peptide synthetase SEQ ID NO:107 68585 oxidase (NRPS-0, blmlll) comparison R: TCACGGGCTCACCTCGT 22 orf-17 57901- Peptide synthetase (NRPS-0, blmlll) comparison R: TCACGGGGCCCCGGCCC 23 SEQ ID NO:106 65781 (NRPS-2-1,blmlV) bochemical characterization. R: TCACTCGGTCCACCTCC 24 orf-18 55899- Asparagine synthetase (NRPS-0, blmll) comparison R: TCACCCGGTCACCTCC 24 orf-19 54418- Homolog of hydroxylase-SEQ ID NO:103 57815 comparison R: TCACCCCGGTGCCGC 25 orf-20 53427- Nucleotide-sugar epimerase Gapped-blast F: GTGACACGGCCCTCCC 30 orf-21 51493- Peptide synthetase Gapped-blast F: ATGCGCGGGCCTCCCC 30 orf-21 51493- Peptide synthetase Gapped-blast F: ATGCGCGGGCACGCCC 29 organison R: TCAGCCACCGTTGCCGC 29 organison R: TCAGCCACCGTGGCC 29 organison R: TCAGCCACCGTTGCCGC 29 organison R: TCAGCCACCGTTGCCGC 29 organison R: TCAGCCACCGTTGCCCC 30 organison R: TCAGCCACCGTTGCCCC 30 organison R: TCAGCCACCGTTGCCCC 30 organison R: TCAGCCACCGTGGCC 30 organison R: TCAGCCACCGTGGCCC 30 organison R: TCAGCCACCGGCCCCCCCCCCGGCCCCCCCCCCCCCCCC		71618-			F: ATGACCACCCCATGACC	13
orf-13 SEQ ID NO:110 71546 Synthesis of mycobactin orf-14 SEQ ID NO:109 70986 Orf-15 SEQ ID NO:109 Orf-15 SEQ ID NO:108 Orf-16 SEQ ID NO:107 Orf-16 SEQ ID NO:107 SEQ ID NO:107 Orf-17 SEQ ID NO:107 SEQ ID NO:108 Orf-18 SEQ ID NO:106 SF81 Orf-18 SEQ ID NO:106 SF899- SEQ ID NO:105 SF815 Orf-19 SF80 ID NO:105 SF815 Orf-19 SF80 ID NO:104 SF80 ID NO:105 SF815 Orf-19 SF80 ID NO:105 SF815 Orf-19 SF80 ID NO:105 SF815 Orf-19 SF80 ID NO:104 SF80 ID NO:105 SF80 ID NO:105 SF815 Orf-19 SF80 ID NO:105 SF815 Orf-19 SF80 ID NO:104 SF80 ID NO:105 SF80 ID	SEQ ID NO:111	72790			R: TCATGGGGTACTCCTGAT	14
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orf-14 SEQ ID NO:109 70986					R: TCAGGTGCCGGACACGCG	16
SEQ ID NO:109 70986 (condensation, blmll) comparison¹ R: TCATCGGTGGCTCCTCGT 18 orf-15 68582- Regulatory gene (homolog SEQ ID NO:108 69601 of syrP) comparison¹ R: TCACGCGCACGGCCCC 19 orf-16 65778- Mutated peptide synthetase- oxidase (NRPS-0, blmlll) comparison¹ R: TCACGGGGCCCGGCCC 21 orf-17 57901- Peptide synthetase (NRPS-0, blmlll) comparison¹ R: TCACGGGGCCTCGTGCG 22 orf-18 5589- Asparagine synthetase (NRPS-2-1,blmlV) bochemical characterization.² orf-18 5589- SEQ ID NO:105 57815 Gapped-blast comparison¹ R: TCACTCCGGTCGCCC 26 orf-19 54418- Homolog of hydroxylase- SEQ ID NO:104 55902 dehydrogenase (blmF) comparison¹ R: TCACTCCCCGGTGCCGC 28 orf-20 53427- Nucleotide-sugar epimerase SEQ ID NO:103 54404 (blmG) comparison R: TCAGGCGGCCCTCC 30 orf-21 51493- Peptide synthetase Gapped-blast comparison R: TCAGGCGGCCCTCCC 30 orf-21 51493- Peptide synthetase Gapped-blast F: ATGCGGGGCCTCCC 30					F: GTGACCGCCCCGGCACA	17
orf-15 SEQ ID NO:108 69601 of syrP) comparison¹ R: TCACGCGCTCACCTCGTC 20 orf-16 SEQ ID NO:107 68585 oxidase (NRPS-0, blmlII) orf-17 SEQ ID NO:106 65781 Orf-18 SEQ ID NO:105 SEQ ID NO:105 SEQ ID NO:105 Orf-19 SEQ ID NO:105 SEQ ID NO:105 SEQ ID NO:106 SS89- SEQ ID NO:105 SEQ ID NO:104 SEQ ID NO:104 SEQ ID NO:105 SEQ ID NO:105 SEQ ID NO:104 SEQ ID NO:105 SEQ ID NO:105 SEQ ID NO:105 SEQ ID NO:104 SEQ ID NO:105 SEQ ID NO:10					R: TCATCGGTGGCTCCTCGT	18
SEQ ID NO:108 69601 of syrP) comparison¹ R: TCACGCGCTCACCTCGTC 20 orf-16 65778- Mutated peptide synthetase- SEQ ID NO:107 68585 oxidase (NRPS-0, blmIII) comparison¹ R: TCACGGGCCCGGCCC 21 SEQ ID NO:107 68585 oxidase (NRPS-0, blmIII) comparison¹ R: TCACGGGGCCCGGCCC 22 orf-17 57901- Peptide synthetase (NRPS-2-1,blmIV) bochemical characterization.² orf-18 55899- Asparagine synthetase Gapped-blast comparison¹ R: TCACTCCGGTCCACCTCC 24 orf-19 54418- Homolog of hydroxylase- SEQ ID NO:104 55902 dehydrogenase (blmF) comparison¹ R: TCACTCCCGGTGCGGC 28 orf-20 53427- Nucleotide-sugar epimerase Gapped-blast SEQ ID NO:103 54404 (blmG) comparison R: TCAGGCACTGGCCGC 30 orf-21 51493- Peptide synthetase Gapped-blast F: ATGCGCGGCCTCCC 30			`			
SEQ ID NO:108 69601 of syrP) comparison R: TCACGCGCTCACCTCGTC 20 orf-16 65778- Mutated peptide synthetase- SEQ ID NO:107 68585 oxidase (NRPS-0, blmIII) comparison R: TCACGGGGCCCGGCCC 21 orf-17 57901- Peptide synthetase Expression and SEQ ID NO:106 65781 (NRPS-2-1,blmIV) biochemical characterization. R: TCACGCGCCCGCCC 24 orf-18 55899- Asparagine synthetase Gapped-blast comparison R: TCACGCGCCCGCC 25 SEQ ID NO:105 57815 Gapped-blast F: GTGAGGCCCGTGTGCGCC 26 orf-19 54418- Homolog of hydroxylase- SEQ ID NO:104 55902 dehydrogenase (blmF) comparison R: TCACTCCCGGTCCGCC 28 orf-20 53427- Nucleotide-sugar epimerase Gapped-blast SEQ ID NO:103 54404 (blmG) comparison R: TCAGGCACCGTGGCCC 30 orf-21 51493- Peptide synthetase Gapped-blast F: ATGCGCGGGCCTCCC 30	orf-15	68582-	Regulatory gene (homolog	Gapped-blast	F: GTGAACCGGCACGGCCCC	19
orf-16	SEQ ID NO:108	69601			R: TCACGCGCTCACCTCGTC	20
SEQ ID NO:107 68585 oxidase (NRPS-0, blmIII) comparison R: TCACGGGGCCTCCGTGCG 22 orf-17 57901- Peptide synthetase (NRPS-2-1, blmIV) bochemical characterization. R: TCACTCCGGTCCACCTCC 24 characterization. R: TCACTCCGGTCCACCTCC 24 characterization. R: TCACTCCGGTCCACCTCC 24 characterization. R: TCACTCCGGTCCACCTCC 25 SEQ ID NO:105 57815 Comparison R: TCAGCCACCGTTGCCGC 26 orf-19 54418- Homolog of hydroxylase- Gapped-blast F: GTGAAGGACCTCGGCCGG 27 SEQ ID NO:104 55902 dehydrogenase (blmF) comparison R: TCACTCCCCGGTGCCGG 28 orf-20 53427- Nucleotide-sugar epimerase Gapped-blast F: GTGACATGGACCGTGGTG 29 SEQ ID NO:103 54404 (blmG) comparison R: TCAGGCATCGGCCTCC 30 orf-21 51493- Peptide synthetase Gapped-blast F: ATGCGCGGGCATGACGAC 31		65778-	Mutated peptide synthetase-		F: GTGACGAGCGCCCGGCCC	21
orf-17 57901- Peptide synthetase (NRPS-2-1,blmlV) bochemical characterization. ² orf-18 55899- Asparagine synthetase Gapped-blast comparison R: TCACTCCGGTGCGCC 26 orf-19 54418- Homolog of hydroxylase- Gapped-blast comparison R: TCACTCCCGGTGCGCC 27 SEQ ID NO:104 55902 dehydrogenase (blmF) comparison R: TCACTCCCCGGTGCGC 28 Orf-20 53427- Nucleotide-sugar epimerase SEQ ID NO:103 54404 (blmG) comparison R: TCAGGCATGGCCCC 30 orf-21 51493- Peptide synthetase Gapped-blast F: ATGCGCGGGCCTCCC 30	SEQ ID NO:107				R: TCACGGGGCCTCCGTGCG	22
SEQ ID NO:106 65781 (NRPS-2-1,blmlV) bochemical characterization. ² orf-18 55899- Asparagine synthetase Gapped-blast comparison R: TCACTCCGGTCCACCTCC 25 SEQ ID NO:105 57815 Gapped-blast F: GTGAGGCCCGTTGCCGCC 26 orf-19 54418- Homolog of hydroxylase- Gapped-blast F: GTGAAGGACCTCGGCCGG 27 SEQ ID NO:104 55902 dehydrogenase (blmF) comparison R: TCACTCCCCGGTGCCGG 28 orf-20 53427- Nucleotide-sugar epimerase Gapped-blast F: GTGACATGGACCGTGGTG 29 SEQ ID NO:103 54404 (blmG) comparison R: TCAGGCATCGGCCCCC 30 orf-21 51493- Peptide synthetase Gapped-blast F: ATGCGCGGGCATGACGAC 31		57901-			F: ATGCTGCACGGCGCCGCG	23
characterization. ² orf-18 SEQ ID NO:105 57815 orf-19 SEQ ID NO:104 55902 orf-20 SEQ ID NO:103 54404 orf-21 SEQ ID NO:103 54404 orf-21 SEQ ID NO:103 54404 characterization. ² Gapped-blast F: GTGAGGCCCGTGTGCGGC 25 Gapped-blast Gapped-blast F: GTGAAGGACCTCGGCCGG 27 Comparison R: TCACTCCCCCGGTGCCGG 28 Gapped-blast F: GTGACATGGACCGTGGTG 29 Comparison R: TCAGGCATCGGCCTGC 29 Comparison R: TCAGGCATCGGCCTCCC 30 Corf-21 51493- Peptide synthetase Gapped-blast F: ATGCGCGGGCCATGACGAC 31	SEQ ID NO:106	65781		biochemical	R: TCACTCCGGTCCACCTCC	24
orf-18 55899- Asparagine synthetase Gapped-blast comparison R: TCAGCCACCGTTGCGGC 25 orf-19 54418- Homolog of hydroxylase- SEQ ID NO:104 55902 dehydrogenase (blmF) comparison R: TCACTCCCCGGTGCGG 28 orf-20 53427- Nucleotide-sugar epimerase Gapped-blast comparison R: TCACTCCCCGGTGCGG 29 SEQ ID NO:103 54404 (blmG) comparison R: TCAGGCATCGGCCGC 30 orf-21 51493- Peptide synthetase Gapped-blast F: ATGCGCGGGCATGACGAC 31	`		, ,	characterization. ²		
SEQ ID NO:105 57815 comparison R: TCAGCCACCGTTGCCGCC 26 orf-19 54418- Homolog of hydroxylase- SEQ ID NO:104 55902 dehydrogenase (blmF) comparison R: TCACTCCCCGGTGCCGG 27 orf-20 53427- Nucleotide-sugar epimerase Gapped-blast comparison R: TCAGTCCCCGGTGCTGG 29 SEQ ID NO:103 54404 (blmG) comparison R: TCAGGCATCGGCCTCCC 30 orf-21 51493- Peptide synthetase Gapped-blast F: ATGCGCGGGCATGACGAC 31	orf-18	55899-	Asparagine synthetase		F: GTGAGGCCCGTGTGCGGC	25
orf-19 54418- Homolog of hydroxylase- Gapped-blast F: GTGAAGGACCTCGGCCGG 27 SEQ ID NO:104 55902 dehydrogenase (blmF) comparison R: TCACTCCCCGGTGCCGG 28 orf-20 53427- Nucleotide-sugar epimerase Gapped-blast comparison R: TCAGGCATGGACCGTGGTG 29 SEQ ID NO:103 54404 (blmG) R: TCAGGCATCGGCCCTCCC 30 orf-21 51493- Peptide synthetase Gapped-blast F: ATGCGCGGGCATGACGAC 31	SEQ ID NO:105	57815			R: TCAGCCACCGTTGCCGCC	26
SEQ ID NO:10455902dehydrogenase (blmF)comparison¹R: TCACTCCCCGGTGCCGG28orf-2053427-Nucleotide-sugar epimeraseGapped-blastF: GTGACATGGACCGTGGTG29SEQ ID NO:10354404(blmG)comparisonR: TCAGGCATCGGCCCTCCC30orf-2151493-Peptide synthetaseGapped-blastF: ATGCGCGGGCATGACGAC31		54418-	Homolog of hydroxylase-		F: GTGAAGGACCTCGGCCGG	27
orf-20 53427- Nucleotide-sugar epimerase Gapped-blast F: GTGACATGGACCGTGGTG 29 SEQ ID NO:103 54404 (blmG) R: TCAGGCATCGGCCCTCCC 30 orf-21 51493- Peptide synthetase Gapped-blast F: ATGCGCGGGCATGACGAC 31	SEQ ID NO:104	55902			R: TCACTCCCCGGTGCCGG	28
SEQ ID NO:10354404(blmG)comparisonR: TCAGGCATCGGCCCTCCC30orf-2151493-Peptide synthetaseGapped-blastF: ATGCGCGGGCATGACGAC31		53427-	Nucleotide-sugar epimerase		F: GTGACATGGACCGTGGTG	29
orf-21 51493- Peptide synthetase Gapped-blast F: ATGCGCGGGCATGACGAC 31	SEQ ID NO:103	54404			R: TCAGGCATCGGCCCTCCC	30
						31
	SEQ ID NO:102	53430	(NRPS-3CT, $blmV$)	comparison ¹	R: TCACGGTGTCTCTCCCTC	32
						33
						34
characterization. ²			, ,		\	
	orf-23	39610-	Peptide synthetase		F GTGACCACGCCCCGCATC	35
						36
characterization. ²		. —	, -,,			

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